Amendments to the Specification

Please replace the paragraph at page 8, lines 3-17, with the following amended paragraph:

A family of homologous proteins (hereinafter referred to as "Protein Cluster II") was identified by an "all-versus-all" BLAST procedure using all Caenorhabditis elegans proteins in the Wormpep20 database release ~~(http://www.sanger.ac.uk/Projects/C_elegans/wormpep/index.shtml)~~ (sanger.ac.uk/Projects/C_elegans/wormpep/index.html). The Wormpep database contains the predicted proteins from the C. elegans genome sequencing project, carried out jointly by the Sanger Centre in Cambridge, UK and the Genome Sequencing Center in St. Louis, USA. A number of 18,940 proteins were retrieved from Wormpep20. The proteins were used in a Smith-Waterman clustering procedure to group together proteins of similarity (Smith T. F. & Waterman M. S. (1981) Identification of common molecular subsequences. J. Mol. Biol. 147(1): 195-197; Pearson W R. (1991) Searching protein sequence libraries: comparison of the sensitivity and selectivity of the Smith-Waterman and FASTA algorithms. Genomics 11: 635-650; Olsen et al. (1999) Optimizing Smith-Waterman alignments. Pac Symp Biocomput.302-313). Completely annotated proteins were filtered out, whereby 10,130 proteins of unknown function could be grouped into 1,800 clusters.

Please replace the paragraph at page 8, lines 18-28, with the following amended paragraph:

The obtained sequence clusters were compared to the Drosophila melanogaster proteins contained in the database Flybase (Berkeley Drosophila Genome Project; ~~http://www.fruitfly.org)~~ fruitfly.org), and annotated clusters were removed. Non-annotated

protein clusters, conserved in both C. elegans and D. melanogaster, were saved to a worn/fly data set, which was used in a BLAST procedure ~~(http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/information3.html)~~ (ncbi.nlm.nih.gov/Education/BLASTinfo/information3.html) against the Celera Human Genome Database ~~(http://www.celera.com)~~ (celera.com). Overlapping fragments were assembled to, as close as possible, full-length proteins using the PHRAP software, developed at the University of Washington ~~(http://www.genome.washington.edu/UWGC/analysistools/phrap.htm)~~ (genome.washington.edu/UWGC/analysistools/phrap.htm). A group of homologous proteins ("Protein Cluster II") with unknown function was chosen for further studies.

Please replace the paragraph at page 9, lines 1-3, with the following amended paragraph:

EST databases provided by the EMBL ~~(http://www.embl.org/Services/index.html)~~ (embl.org/Services/index.html) were used to check whether the human proteins in Cluster II were expressed, in order to identify putative pseudogenes. One putative pseudogene was identified and excluded.

Please replace the paragraph at page 9, line 19 -- page 10, line 7, with the following amended paragraph:

A HMM-Pfam search was performed on the human family members. Pfam is a large collection of protein families and domains. Pfam contains multiple protein alignments and profile-HMMs (Profile Hidden Markov Models) of these families. Profile-HMMs can be used to do sensitive database searching using statistical descriptions of a sequence family's consensus. Pfam is available on the WWW at ~~http://pfam.wustl.edu; http://www.sanger.ac.uk/Software/Pfam; and http://www.cgr.ki.se/Pfam~~. pfam.wustl.edu;

sanger.ac.uk/Software/Pfam; and cgr.ki.se/Pfam. The latest version (4.3) of Pfam contains 1815 families. These Pfam families match 63% of proteins in SWISS-PROT 37 and TrEMBL 9. For references to Pfam, see Bateman et al. (2000) The Pfam protein families database. Nucleic Acids Res. 28:263-266; Sonnhammer et al. (1998) Pfam: Multiple Sequence Alignments and HMM-Profiles of Protein Domains. Nucleic Acids Research, 26:322-325; Sonnhammer et al. (1997) Pfam: a Comprehensive Database of Protein Domain Families Based on Seed Alignments. Proteins 28:405-420.

Please replace the paragraph at page 10, lines 12-18, with the following amended paragraph:

A Pfam-B search revealed identity to the Pfam-B 7357 domain (Pfam Accession No. PB007357). Pfam-B domains are generated automatically from an alignment taken from the database ProDom 2000.1 ~~(http://www.lunix.toulouse.inra.fr/prodom)~~ (lunix.toulouse.inra.fr/prodom) subtracting sequence segments already covered by Pfam-A. The ProDom database has been designed as tool to help analyze domain arrangements of proteins and protein families (Corpet et al. (1999) Nucleic Acid Research 27: 263-267). Pfam-B domains are curated manually at the Sanger Centre, UK, to become Pfam-A domains.

Please replace the paragraph at page 10, lines 20-25, with the following amended paragraph:

The human proteins in Cluster II were analyzed using the TM-HMM tool available e.g. at ~~http://www.cbs.dtu.dk/services/TMHMM-1.0~~ cbs.dtu.dk/services/TMHMM-1.0. TM-HMM is a method to model and predict the location and orientation of alpha helices in membrane-spanning proteins (Sonnhammer et al. (1998) A hidden Markov model for

predicting transmembrane helices in protein sequences. ISMB 6:175-182). No transmembrane regions were identified.

Please replace the paragraph at page 11, lines 17-23, with the following amended paragraph:

The tissue distribution of the human genes was studied using the Incyte ~~LifeSeq®~~ LIFESEQ® database ~~(http://www.incyte.com)~~ (incyte.com). The nucleic acid molecules shown as SEQ ID NO: 1, 3 and 5 were found to be expressed primarily in germ cells and in the nervous system. Therefore, the said nucleic acid molecules shown as SEQ ID NO: 1, 3 and 5 and the polypeptides shown as SEQ ID NO: 2, 4 and 6 are proposed to be useful for differential identification of the tissue(s) or cell types(s) present in a biological sample and for diagnosis of diseases and disorders, including disorders of the central nervous system.

Please replace the paragraph at page 12, lines 2-8, with the following amended paragraph:

Multiple Tissue Northern blotting (MTN) is performed to make a more thorough analysis of the expression profiles of the proteins in Cluster II. Multiple Tissue Northern (MTN™) Blots ~~(http://www.clontech.com/mtn)~~ (clontech.com/mtn) are pre-made Northern blots featuring Premium Poly A+ RNA from a variety of different human, mouse, or rat tissues. MTN Blots can be used to analyze size and relative abundance of transcripts in different tissues. MTN Blots can also be used to investigate gene families and alternate splice forms and to assess cross species homology.

Please replace the paragraph at page 12, lines 16-26, with the following amended paragraph:

The expression pattern of the proteins in Cluster II can be analyzed using ~~GeneChip®~~ GENECHIP® expression arrays ~~(http://www.affymetrix.com /products/app_exp.html)~~ (affymetrix.com/products/app_exp.html). Briefly, mRNAs are extracted from various tissues. They are reverse transcribed using a T7-tagged oligo-dT primer and double-stranded cDNAs are generated. These cDNAs are then amplified and labeled using In Vitro Transcription (IVT) with T7 RNA polymerase and biotinylated nucleotides. The populations of cRNAs obtained are purified and fragmented by heat to produce a distribution of RNA fragment sizes from approximately 35 to 200 bases. ~~GeneChip®~~ GENECHIP® expression arrays are hybridized with the samples. The arrays are washed and stained. The cartridges are scanned using a confocal scanner and the images are analyzed with the GeneChip 3.1 software (Affymetrix).

Please replace the paragraph at page 13, lines 8-18, with the following amended paragraph:

The two-hybrid method can be used to determine if two known proteins (i.e. proteins for which the corresponding genes have been previously cloned) interact. Another important application of the two-hybrid method is to identify previously unknown proteins that interact with a target protein by screening a two-hybrid library. For reviews, see e.g.: Chien et al. (1991) The two-hybrid system: a method to identify and clone genes for proteins that interact with a protein of interest. Proc. Natl. Acad. Sci. U.S.A. 88:9578-9582; Bartel P L, Fields (1995) Analyzing protein-protein interactions using two-hybrid system. Methods Enzymol. 254:241-263; or Wallach et al. (1998) The yeast two-hybrid screening technique and its use in the study of protein-protein interactions in apoptosis. Curr. Opin. Immunol. 10(2): 131-136. See also ~~http://www.clontech.com/matchmaker~~ clontech.com/matchmaker.